



50508-2200

SEQUENCE LISTING

<110> Emory University

<120> Mammalian Cell Lines Specifically Deficient in O-Linked Glycosylation

<130> 050508-2200

<150> 60/455,365

<151> 2003-03-17

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 1047

<212> DNA

<213> Homo Sapiens

<400> 1

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120

ggagggggct ccctgcctga gagcctgcgg cgggtccagg agctgacagg ccgctctgtg
180

gagtttgagg agatggacat tttggaccag ggagccctac agcgtctctt caaaaagtac
240

agctttatgg cggtcaccca ctttgccggg ctcaaggccg tgggcgagtc ggtgcagaag
300

cctctggatt attacagagt taacctgacc gggaccatcc agcttctgga gatcatgaag
360

gcccacgggg tgaagaacct ggtgttcagc agctcagcca ctgtgtacgg gaacccccag
420

tacctgcccc ttgatgaggc ccaccccacg ggtggttgta ccaaccctta cggcaagtcc
480

aagttcttca tcgaggaaat gatccgggac ctgtgccagg cagacaagac ttggaacgca
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gtgctgctgc gctatttcaa cccacaggt gccatgcct ctggctgcat tggtaggat
600

cccagggca tacccaacaa cctcatgcct tatgtctccc aggtggcgat cgggcgacgg
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720

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840

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gaaggtgatg tggcagccta ttacgccaac ccagcctgg cccaagagga gctgggggtg
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<210> 2
<211> 348
<212> PRT
<213> Human polypeptide

<400> 2

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His	Thr	Val	Leu	Glu	Leu	Leu	Glu	Ala	Gly	Tyr	Leu	Pro	Val	Val	Ile
			20					25					30		

Asp	Asn	Phe	His	Asn	Ala	Phe	Arg	Gly	Gly	Gly	Ser	Leu	Pro	Glu	Ser
		35					40						45		

Leu Arg Arg Val Gln Glu Leu Thr Gly Arg Ser Val Glu Phe Glu Glu
 50 55 60

Met Asp Ile Leu Asp Gln Gly Ala Leu Gln Arg Leu Phe Lys Lys Tyr
 65 70 75 80

Ser Phe Met Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu
 85 90 95

Ser Val Gln Lys Pro Leu Asp Tyr Tyr Arg Val Asn Leu Thr Gly Thr
 100 105 110

Ile Gln Leu Leu Glu Ile Met Lys Ala His Gly Val Lys Asn Leu Val
 115 120 125

Phe Ser Ser Ser Ala Thr Val Tyr Gly Asn Pro Gln Tyr Leu Pro Leu
 130 135 140

Asp Glu Ala His Pro Thr Gly Gly Cys Thr Asn Pro Tyr Gly Lys Ser
 145 150 155 160

Lys Phe Phe Ile Glu Glu Met Ile Arg Asp Leu Cys Gln Ala Asp Lys
 165 170 175

Thr Trp Asn Ala Val Leu Leu Arg Tyr Phe Asn Pro Thr Gly Ala His
 180 185 190

Ala Ser Gly Cys Ile Gly Glu Asp Pro Gln Gly Ile Pro Asn Asn Leu
 195 200 205

Met Pro Tyr Val Ser Gln Val Ala Ile Gly Arg Arg Glu Ala Leu Asn
 210 215 220

Val Phe Gly Asn Asp Tyr Asp Thr Glu Asp Gly Thr Gly Val Arg Asp
 225 230 235 240

Tyr Ile His Val Val Asp Leu Ala Lys Gly His Ile Ala Ala Leu Arg
 245 250 255

Lys Leu Lys Glu Gln Cys Gly Cys Arg Ile Tyr Asn Leu Gly Thr Gly
 260 265 270

Thr Gly Tyr Ser Val Leu Gln Met Val Gln Ala Met Glu Lys Ala Ser
 275 280 285

Gly Lys Lys Ile Pro Tyr Lys Val Val Ala Arg Arg Glu Gly Asp Val
 290 295 300

Ala Ala Tyr Tyr Ala Asn Pro Ser Leu Ala Gln Glu Glu Leu Gly Trp
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Thr Ala Ala Leu Gly Leu Asp Arg Met Cys Glu Asp Leu Trp Arg Trp
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Gln Lys Gln Asn Pro Ser Gly Phe Gly Thr Gln Ala
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<210> 3

<211> 1017

<212> DNA

<213> Eschenichia coli

<400> 3

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 120

ctgcctgtta tcgagcgttt aggcggcaaa catccaacgt ttgttgaagg cgatattcgt
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aacgaagcgt tgatgaccga gatacctgcac gatcacgcta tcgacaccgt gatccacttc
 240

gccgggctga aagccgtggg cgaatcggta caaaaaccgc tggaatatta cgacaacaat
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gtcaacggca ctctgcgct gattagcgcc atgcgcgccc ctaacgtcaa aaactttatt
360

tttagctcct ccgccaccgt ttatggcgat cagcccaaaa ttccatacgt tgaaagcttc
420

ccgaccggca caccgcaaag cccttacggc aaaagcaagc tgatgggtgga acagatcctc
480

accgatctgc aaaaagccca gccggactgg agcattgccc tgctgcgcta cttcaaccgg
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gttggcgcgc atccgtcggg cgatatgggc gaagatccgc aaggcattcc gaataacctg
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660

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720

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780

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900

gcggacgcca gcaaagccga ccgtgaactg aactggcgcg taacgcgcac actcgatgaa
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1017

<210> 4

<211> 338

<212> PRT

<213> Eschesichia Coli

<400> 4

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Cys Val Gln Leu Leu Gln Asn Gly His Asp Val Ile Ile Leu Asp Asn
 20 25 30

Leu Cys Asn Ser Lys Arg Ser Val Leu Pro Val Ile Glu Arg Leu Gly
 35 40 45

Gly Lys His Pro Thr Phe Val Glu Gly Asp Ile Arg Asn Glu Ala Leu
 50 55 60

Met Thr Glu Ile Leu His Asp His Ala Ile Asp Thr Val Ile His Phe
 65 70 75 80

Ala Gly Leu Lys Ala Val Gly Glu Ser Val Gln Lys Pro Leu Glu Tyr
 85 90 95

Tyr Asp Asn Asn Val Asn Gly Thr Leu Arg Leu Ile Ser Ala Met Arg
 100 105 110

Ala Ala Asn Val Lys Asn Phe Ile Phe Ser Ser Ser Ala Thr Val Tyr
 115 120 125

Gly Asp Gln Pro Lys Ile Pro Tyr Val Glu Ser Phe Pro Thr Gly Thr
 130 135 140

Pro Gln Ser Pro Tyr Gly Lys Ser Lys Leu Met Val Glu Gln Ile Leu
 145 150 155 160

Thr Asp Leu Gln Lys Ala Gln Pro Asp Trp Ser Ile Ala Leu Leu Arg
 165 170 175

Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly Asp Met Gly Glu Asp
 180 185 190

Pro Gln Gly Ile Pro Asn Asn Leu Met Pro Tyr Ile Ala Gln Val Ala
 195 200 205

Val Gly Arg Arg Asp Ser Leu Ala Ile Phe Gly Asn Asp Tyr Pro Thr
 210 215 220

Glu Asp Gly Thr Gly Val Arg Asp Tyr Ile His Val Met Asp Leu Ala
 225 230 235 240

Asp Gly His Val Val Ala Met Glu Lys Leu Ala Asn Lys Pro Gly Val
 245 250 255

His Ile Tyr Asn Leu Gly Ala Gly Val Gly Asn Ser Val Leu Asp Val
 260 265 270

Val Asn Ala Phe Ser Lys Ala Cys Gly Lys Pro Val Asn Tyr His Phe
 275 280 285

Ala Pro Arg Arg Glu Gly Asp Leu Pro Ala Tyr Trp Ala Asp Ala Ser
 290 295 300

Lys Ala Asp Arg Glu Leu Asn Trp Arg Val Thr Arg Thr Leu Asp Glu
 305 310 315 320

Met Ala Gln Asp Thr Trp His Trp Gln Ser Arg His Pro Gln Gly Tyr
 325 330 335

Pro Asp

<210> 5
 <211> 30
 <212> DNA
 <213> Human DNA

<400> 5
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<210> 6

<211> 33
<212> DNA
<213> Human DNA

<400> 6
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<210> 7
<211> 40
<212> DNA
<213> Mouse DNA

<400> 7
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<210> 8
<211> 37
<212> DNA
<213> Mouse DNA

<400> 8
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